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| (71) Applicant: GENETICS INSTITUTE, INC. [US/US]; 87 CambridgePark Drive, Cambridge, MA 02140 (US). | | | |
| (72) Inventors: MERBERG, David; 2 Orchard Drive, Acton, MA 01720 (US). MCCOY, John, M.; 56 Howard Street, Reading, MA 01867 (US). LAVALLIE, Edward, R.; 90 Green Meadow Drive, Tewksbury, MA 01876 (US). RACIE, Lisa, A.; 124 School Street, Acton, MA 01720 (US). TREACY, Maurice; 93 Walcott Road, Chestnut Hill, MA 02167 (US). SPAULDING, Vikki; 11 Meadowbank Road, Billerica, MA 01821 (US). JACOBS, Kenneth; 151 Beaumont Avenue, Newton, MA 02160 (US). | | | |
| (74) Agent: SPRUNGER, Suzanne, A.; Genetics Institute, Inc., 87 CambridgePark Drive, Cambridge, MA 02140 (US). | | | |
| (54) Title: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM | | | |
| (57) Abstract Novel polynucleotides and the proteins encoded thereby are disclosed. | | | |

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SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

5 FIELD OF THE INVENTION

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins.

10 BACKGROUND OF THE INVENTION

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity by virtue of their secreted nature in the case of leader sequence cloning, or by virtue of the cell or tissue source in the case of PCR-based techniques. It is to these proteins and the polynucleotides encoding them that the present invention is directed.

25 SUMMARY OF THE INVENTION

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 NO:1;
- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
- NO:1 from nucleotide 593 to nucleotide 949;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1
- from nucleotide 650 to nucleotide 949;
- 35 (d) a polynucleotide comprising the nucleotide sequence of the full length
- protein coding sequence of clone AY421_2 deposited under accession number ATCC
- 98145;

- (e) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AY421_2 deposited under accession number ATCC 98145;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AY421_2 deposited under accession number ATCC 98145;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AY421_2 deposited under accession number ATCC 98145;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above .

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:1 from nucleotide 593 to nucleotide 949; the nucleotide sequence of SEQ ID NO:1 from nucleotide 650 to nucleotide 949; the nucleotide sequence of the full length protein coding sequence of clone AY421_2 deposited under accession number ATCC 98145; or the nucleotide sequence of the mature protein coding sequence of clone AY421_2 deposited under accession number ATCC 98145. In other preferred embodiments, the polynucleotide encodes the full length or mature protein encoded by the cDNA insert of clone AY421_2 deposited under accession number ATCC 98145.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:1 or SEQ ID NO:.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:2;
- (b) fragments of the amino acid sequence of SEQ ID NO:2; and
- (c) the amino acid sequence encoded by the cDNA insert of clone AY421_2 deposited under accession number ATCC 98145;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:2.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 271 to nucleotide 498;
- (c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone BV278_2 deposited under accession number ATCC 98145;
- 10 (d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone BV278_2 deposited under accession number ATCC 98145;
- (e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone BV278_2 deposited under accession number ATCC 98145;
- 15 (f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone BV278_2 deposited under accession number ATCC 98145;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:6;
- (h) a polynucleotide encoding a protein comprising a fragment of the
20 amino acid sequence of SEQ ID NO:6 having biological activity;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(d) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above .

25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:5 from nucleotide 271 to nucleotide 498; the nucleotide sequence of the full length protein coding sequence of clone BV278_2 deposited under accession number ATCC 98145; or the nucleotide sequence of the mature protein coding sequence of clone BV278_2 deposited under accession number ATCC 98145. In other preferred embodiments, the polynucleotide encodes
30 the full length or mature protein encoded by the cDNA insert of clone BV278_2 deposited under accession number ATCC 98145.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:5, SEQ ID NO:4 or SEQ ID NO:7 .

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:6;
- 5 (b) fragments of the amino acid sequence of SEQ ID NO:6; and
- (c) the amino acid sequence encoded by the cDNA insert of clone BV278_2 deposited under accession number ATCC 98145;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:6.

10 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:8;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:8
15 from nucleotide 36 to nucleotide 722;
- (c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone C544_1 deposited under accession number ATCC 98145;
- (d) a polynucleotide encoding the full length protein encoded by the
20 cDNA insert of clone C544_1 deposited under accession number ATCC 98145;
- (e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone C544_1 deposited under accession number ATCC 98145;
- (f) a polynucleotide encoding the mature protein encoded by the cDNA
25 insert of clone C544_1 deposited under accession number ATCC 98145;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:9;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:9 having biological activity;
- 30 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(d) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:8
35 from nucleotide 36 to nucleotide 722; the nucleotide sequence of the full length protein coding

sequence of clone C544_1 deposited under accession number ATCC 98145; or the nucleotide sequence of the mature protein coding sequence of clone C544_1 deposited under accession number ATCC 98145. In other preferred embodiments, the polynucleotide encodes the full length or mature protein encoded by the cDNA insert of clone C544_1 deposited under
5 accession number ATCC 98145. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:9 from amino acid 101 to amino acid 185.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:8 or SEQ ID NO:.

10 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:9;
- (b) the amino acid sequence of SEQ ID NO:9 from amino acid 101 to
15 amino acid 185;
- (c) fragments of the amino acid sequence of SEQ ID NO:9; and
- (d) the amino acid sequence encoded by the cDNA insert of clone C544_1 deposited under accession number ATCC 98145;

the protein being substantially free from other mammalian proteins. Preferably such protein
20 comprises the amino acid sequence of SEQ ID NO:9 or the amino acid sequence of SEQ ID NO:9 from amino acid 101 to amino acid 185.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
25 NO:12;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:12 from nucleotide 34 to nucleotide 249;
- (c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone CC332_33 deposited under accession number ATCC
30 98145;
- (d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone CC332_33 deposited under accession number ATCC 98145;
- (e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone CC332_33 deposited under accession number ATCC
35 98145;

(f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone CC332_33 deposited under accession number ATCC 98145;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:13;

5 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:13 having biological activity;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(d) above;

10 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above .

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:12 from nucleotide 34 to nucleotide 249; the nucleotide sequence of the full length protein coding sequence of clone CC332_33 deposited under accession number ATCC 98145; or the nucleotide sequence of the mature protein coding sequence of clone CC332_33 deposited under accession number ATCC 98145. In other preferred embodiments, the polynucleotide encodes the full length or mature protein encoded by the cDNA insert of clone CC332_33 deposited under accession number ATCC 98145.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:12, SEQ ID NO:11 or SEQ ID NO:14 .

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:13;

(b) fragments of the amino acid sequence of SEQ ID NO:13; and

25 (c) the amino acid sequence encoded by the cDNA insert of clone CC332_33 deposited under accession number ATCC 98145;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:13.

30 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 89 to nucleotide 436;

- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 212 to nucleotide 436;
- (d) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone CC365_40 deposited under accession number ATCC 98145;
- (e) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone CC365_40 deposited under accession number ATCC 98145;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone CC365_40 deposited under accession number ATCC 98145;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone CC365_40 deposited under accession number ATCC 98145;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above .

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:15 from nucleotide 89 to nucleotide 436; the nucleotide sequence of SEQ ID NO:15 from nucleotide 212 to nucleotide 436; the nucleotide sequence of the full length protein coding sequence of clone CC365_40 deposited under accession number ATCC 98145; or the nucleotide sequence of the mature protein coding sequence of clone CC365_40 deposited under accession number ATCC 98145. In other preferred embodiments, the polynucleotide encodes the full length or mature protein encoded by the cDNA insert of clone CC365_40 deposited under accession number ATCC 98145. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16 from amino acid 17 to amino acid 116.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:15 or SEQ ID NO:16.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:16;
- (b) the amino acid sequence of SEQ ID NO:16 from amino acid 17 to amino acid 116;
- (c) fragments of the amino acid sequence of SEQ ID NO:16; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CC365_40 deposited under accession number ATCC 98145;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:16 or the amino acid sequence of SEQ ID NO:16 from amino acid 17 to amino acid 116.

10 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:18;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:18 from nucleotide 769 to nucleotide 966;
- (c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone CG68_4 deposited under accession number ATCC 98145;
- (d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone CG68_4 deposited under accession number ATCC 98145;
- (e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone CG68_4 deposited under accession number ATCC 98145;
- (f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone CG68_4 deposited under accession number ATCC 98145;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:19;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:19 having biological activity;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(d) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:18 from nucleotide 769 to nucleotide 966; the nucleotide sequence of the full length protein

coding sequence of clone CG68_4 deposited under accession number ATCC 98145; or the nucleotide sequence of the mature protein coding sequence of clone CG68_4 deposited under accession number ATCC 98145. In other preferred embodiments, the polynucleotide encodes the full length or mature protein encoded by the cDNA insert of clone CG68_4 deposited under
5 accession number ATCC 98145. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:19 from amino acid 18 to amino acid 57.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:18.

10 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:19;
- (b) the amino acid sequence of SEQ ID NO:19 from amino acid 18 to
15 amino acid 57;
- (c) fragments of the amino acid sequence of SEQ ID NO:19; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CG68_4 deposited under accession number ATCC 98145;

the protein being substantially free from other mammalian proteins. Preferably such protein
20 comprises the amino acid sequence of SEQ ID NO:19 or the amino acid sequence of SEQ ID NO:19 from amino acid 18 to amino acid 57.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
25 NO:20;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:20 from nucleotide 1042 to nucleotide 1389;
- (c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone D329_1 deposited under accession number ATCC
30 98145;
- (d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone D329_1 deposited under accession number ATCC 98145;
- (e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone D329_1 deposited under accession number ATCC
35 98145;

(f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone D329_1 deposited under accession number ATCC 98145;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:21;

5 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:21 having biological activity;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(d) above;

10 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above .

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:20 from nucleotide 1042 to nucleotide 1389; the nucleotide sequence of the full length protein coding sequence of clone D329_1 deposited under accession number ATCC 98145; or the nucleotide sequence of the mature protein coding sequence of clone D329_1 deposited under
15 accession number ATCC 98145. In other preferred embodiments, the polynucleotide encodes the full length or mature protein encoded by the cDNA insert of clone D329_1 deposited under accession number ATCC 98145.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:20 or SEQ ID NO:.

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:21;

(b) fragments of the amino acid sequence of SEQ ID NO:21; and

25 (c) the amino acid sequence encoded by the cDNA insert of clone D329_1 deposited under accession number ATCC 98145;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:21.

30 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:24;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:24 from nucleotide 279 to nucleotide 515;

- (c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone H698_3 deposited under accession number ATCC 98145;
- 5 (d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone H698_3 deposited under accession number ATCC 98145;
- (e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone H698_3 deposited under accession number ATCC 98145;
- 10 (f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone H698_3 deposited under accession number ATCC 98145;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:25;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:25 having biological activity;
- 15 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(d) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above .

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:24 from nucleotide 279 to nucleotide 515; the nucleotide sequence of the full length protein coding sequence of clone H698_3 deposited under accession number ATCC 98145; or the nucleotide sequence of the mature protein coding sequence of clone H698_3 deposited under accession number ATCC 98145. In other preferred embodiments, the polynucleotide encodes the full length or mature protein encoded by the cDNA insert of clone H698_3 deposited under
25 accession number ATCC 98145.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:24, SEQ ID NO:23 or SEQ ID NO:26 .

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group
30 consisting of:

- (a) the amino acid sequence of SEQ ID NO:25;
- (b) fragments of the amino acid sequence of SEQ ID NO:25; and
- (c) the amino acid sequence encoded by the cDNA insert of clone H698_3 deposited under accession number ATCC 98145;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:25.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 199 to nucleotide 1155;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:27 from nucleotide 304 to nucleotide 1155;
- (d) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone H963_20 deposited under accession number ATCC 98145;
- (e) a polynucleotide encoding the full length protein encoded by the
15 cDNA insert of clone H963_20 deposited under accession number ATCC 98145;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone H963_20 deposited under accession number ATCC 98145;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA
20 insert of clone H963_20 deposited under accession number ATCC 98145;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:28;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above .

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:27
30 from nucleotide 199 to nucleotide 1155; the nucleotide sequence of SEQ ID NO:27 from nucleotide 304 to nucleotide 1155; the nucleotide sequence of the full length protein coding sequence of clone H963_20 deposited under accession number ATCC 98145; or the nucleotide sequence of the mature protein coding sequence of clone H963_20 deposited under accession number ATCC 98145. In other preferred embodiments, the polynucleotide encodes the full
35 length or mature protein encoded by the cDNA insert of clone H963_20 deposited under

accession number ATCC 98145. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:28 from amino acid 19 to amino acid 84.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
5 ID NO:27.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:28;
- 10 (b) the amino acid sequence of SEQ ID NO:28 from amino acid 19 to amino acid 84;
- (c) fragments of the amino acid sequence of SEQ ID NO:28; and
- (d) the amino acid sequence encoded by the cDNA insert of clone
H963_20 deposited under accession number ATCC 98145;

15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:28 or the amino acid sequence of SEQ ID NO:28 from amino acid 19 to amino acid 84.

In certain preferred embodiments, the polynucleotide is operably linked to an expression control sequence. The invention also provides a host cell, including bacterial, yeast,
20 insect and mammalian cells, transformed with such polynucleotide compositions.

Processes are also provided for producing a protein, which comprise:

- (a) growing a culture of the host cell transformed with such polynucleotide compositions in a suitable culture medium; and
 - (b) purifying the protein from the culture.
- 25 The protein produced according to such methods is also provided by the present invention. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Protein compositions of the present invention may further comprise a pharmaceutically acceptable carrier. Compositions comprising an antibody which specifically reacts with such
30 protein are also provided by the present invention.

Methods are also provided for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically effective amount of a composition comprising a protein of the present invention and a pharmaceutically acceptable carrier.

35

DETAILED DESCRIPTION

ISOLATED PROTEINS AND POLYNUCLEOTIDES

Nucleotide and amino acid sequences are reported below for each clone and protein disclosed in the present application. In some instances the sequences are preliminary and may include some incorrect or ambiguous bases or amino acids. The actual nucleotide sequence of each clone can readily be determined by sequencing of the deposited clone in accordance with known methods. The predicted amino acid sequence (both full length and mature) can then be determined from such nucleotide sequence. The amino acid sequence of the protein encoded by a particular clone can also be determined by expression of the clone in a suitable host cell, collecting the protein and determining its sequence.

For each disclosed protein applicants have identified what they have determined to be the reading frame best identifiable with sequence information available at the time of filing. Because of the partial ambiguity in reported sequence information, reported protein sequences include "Xaa" designators. These "Xaa" designators indicate either (1) a residue which cannot be identified because of nucleotide sequence ambiguity or (2) a stop codon in the determined nucleotide sequence where applicants believe one should not exist (if the nucleotide sequence were determined more accurately).

As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

Clone "AY421_2"

A polynucleotide of the present invention has been identified as clone "AY421_2". AY421_2 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins. AY421_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AY421_2 protein").

The nucleotide sequence of the 5' portion of AY421_2 as presently determined is reported in SEQ ID NO:1. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:2. The predicted acid sequence of the AY421_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:2. Amino acids 1 to 19 are the predicted leader/signal sequence, with the predicted mature amino

acid sequence beginning at amino acid 20. Additional nucleotide sequence from the 3' portion of AY421_2, including the polyA tail, is reported in SEQ ID NO:3.

The nucleotide sequence disclosed herein for AY421_2 was searched against the GenBank database using BLASTA/BLASTX and FASTA search protocols. AY421_2 demonstrated at least some identity with an EST identified as "yr41b09.r1 Homo sapiens cDNA clone 207833 5'" (H60299, BlastN). Based upon identity, AY421_2 proteins and each identical protein or peptide may share at least some activity. The amino acid sequence of AY421_2 indicates that it has some homology to cytochrome oxidase assembly protein (L38643, BlastX).

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Clone "BV278_2"

A polynucleotide of the present invention has been identified as clone "BV278_2". BV278_2 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins. BV278_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BV278_2 protein").

The nucleotide sequence of the 5' portion of BV278_2 as presently determined is reported in SEQ ID NO:4. An additional internal nucleotide sequence from BV278_2 as presently determined is reported in SEQ ID NO:5. What applicants believe is the proper reading frame and the predicted amino acid sequence encoded by such internal sequence is reported in SEQ ID NO:6. Additional nucleotide sequence from the 3' portion of BV278_2, including the polyA tail, is reported in SEQ ID NO:7.

The nucleotide sequence disclosed herein for BV278_2 was searched against the GenBank database using BLASTA/BLASTX and FASTA search protocols. No hits were found in the database.

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Clone "C544_1"

A polynucleotide of the present invention has been identified as clone "C544_1". C544_1 was isolated from a human PBMC cDNA library using methods which are selective for cDNAs encoding secreted proteins. C544_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "C544_1 protein").

The nucleotide sequence of the 5' portion of C544_1 as presently determined is reported in SEQ ID NO:8. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:9. The predicted acid sequence of the C544_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:9.

Additional nucleotide sequence from the 3' portion of C544_1, including the polyA tail, is reported in SEQ ID NO:10.

The nucleotide sequence disclosed herein for C544_1 was searched against the GenBank database using BLASTA/BLASTX and FASTA search protocols. C544_1 demonstrated at least some identity with ESTs identified as "yd76d07.r1 Homo sapiens cDNA clone 114157 5'" (T85425, BlastN) and "ya98b10.s1 Homo sapiens cDNA clone 69691 3'" (T53653, Fasta). Based upon identity, C544_1 proteins and each identical protein or peptide may share at least some activity.

10 Clone "CC332_33"

A polynucleotide of the present invention has been identified as clone "CC332_33". CC332_33 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins. CC332_33 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CC332_33 protein").

The nucleotide sequence of the 5' portion of CC332_33 as presently determined is reported in SEQ ID NO:11. An additional internal nucleotide sequence from CC332_33 as presently determined is reported in SEQ ID NO:12. What applicants believe is the proper reading frame and the predicted amino acid sequence encoded by such internal sequence is reported in SEQ ID NO:13. Additional nucleotide sequence from the 3' portion of CC332_33, including the polyA tail, is reported in SEQ ID NO:14.

The nucleotide sequence disclosed herein for CC332_33 was searched against the GenBank database using BLASTA/BLASTX and FASTA search protocols. CC332_33 demonstrated at least some identity with an EST identified as "yy61d06.s1 Homo sapiens cDNA clone 278027 3'" (N63467, BlastN). Based upon identity, CC332_33 proteins and each identical protein or peptide may share at least some activity.

25 Clone "CC365_40"

A polynucleotide of the present invention has been identified as clone "CC365_40". CC365_40 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins. CC365_40 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CC365_40 protein").

The nucleotide sequence of the 5' portion of CC365_40 as presently determined is reported in SEQ ID NO:15. What applicants presently believe is the proper reading frame for

the coding region is indicated in SEQ ID NO:16. The predicted acid sequence of the CC365_40 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:16. Amino acids 1 to 41 are the predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 42. Additional nucleotide sequence from
5 the 3' portion of CC365_40, including the polyA tail, is reported in SEQ ID NO:17.

The nucleotide sequence disclosed herein for CC365_40 was searched against the GenBank database using BLASTA/BLASTX and FASTA search protocols. CC365_40 demonstrated at least some identity with a ESTs identified as "58b3 Human retina cDNA Tsp509I-cleaved sublibrary Hommo" (W21840, BlastN) and "EST109372 Rattus sp. cDNA
10 5' end" (H33410, Fasta). Based upon identity, CC365_40 proteins and each identical protein or peptide may share at least some activity.

Clone "CG68_4"

A polynucleotide of the present invention has been identified as clone "CG68_4".
15 CG68_4 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins. CG68_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CG68_4 protein").

The nucleotide sequence of CG68_4 as presently determined is reported in SEQ ID NO:18. What applicants presently believe to be the proper reading frame and the predicted
20 amino acid sequence of the CG68_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:19. .

The nucleotide sequence disclosed herein for CG68_4 was searched against the GenBank database using BLASTA/BLASTX and FASTA search protocols. No hits were found in the database. The amino acid sequence of CG68_4 indicates that have some weak
25 homology at the protein level with the IL-4 receptor (M29854, BlastX).

Clone "D329_1"

A polynucleotide of the present invention has been identified as clone "D329_1". D329_1 was isolated from a human PBMC cDNA library using methods which are selective
30 for cDNAs encoding secreted proteins. D329_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "D329_1 protein").

The nucleotide sequence of the 5' portion of D329_1 as presently determined is reported in SEQ ID NO:20. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:21. The predicted acid sequence of the D329_1
35 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:21.

Additional nucleotide sequence from the 3' portion of D329_1, including the polyA tail, is reported in SEQ ID NO:22.

The nucleotide sequence disclosed herein for D329_1 was searched against the GenBank database using BLASTA/BLASTX and FASTA search protocols. D329_1 demonstrated at least some identity with an EST identified as "zc32g12.r1 Soares senescent fibroblasts NbHSF Homo" (W46599, BlastN). Based upon identity, D329_1 proteins and each identical protein or peptide may share at least some activity.

Clone "H698_3"

A polynucleotide of the present invention has been identified as clone "H698_3". H698_3 was isolated from a human PBMC cDNA library using methods which are selective for cDNAs encoding secreted proteins. H698_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "H698_3 protein").

The nucleotide sequence of the 5' portion of H698_3 as presently determined is reported in SEQ ID NO:23. An additional internal nucleotide sequence from H698_3 as presently determined is reported in SEQ ID NO:24. What applicants believe is the proper reading frame and the predicted amino acid sequence encoded by such internal sequence is reported in SEQ ID NO:25. Additional nucleotide sequence from the 3' portion of H698_3, including the polyA tail, is reported in SEQ ID NO:26.

The nucleotide sequence disclosed herein for H698_3 was searched against the GenBank database using BLASTA/BLASTX and FASTA search protocols. H698_3 demonstrated at least some identity with an EST identified as "zd85h08.r1 Soares fetal heart NbHH19W Homo sapiens cDNA" (W81295, BlastN). Based upon identity, H698_3 proteins and each identical protein or peptide may share at least some activity.

Clone "H963_20"

A polynucleotide of the present invention has been identified as clone "H963_20". H963_20 was isolated from a human PBMC cDNA library using methods which are selective for cDNAs encoding secreted proteins. H963_20 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "H963_20 protein").

The nucleotide sequence of H963_20 as presently determined is reported in SEQ ID NO:27. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the H963_20 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:28. Amino acids 1 to 35 are the predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 36.

The nucleotide sequence disclosed herein for H963_20 was searched against the GenBank database using BLASTA/BLASTX and FASTA search protocols. No hits were found in the database. The amino acid sequence of H963_20 indicates that it may be a G-protein-coupled receptor.

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Deposit of Clones

Clones AY421_2, BV278_2, C544_1, CC332_33, CC365_40, CG68_4, D329_1, H698_3 and H963_20 were deposited on August 21, 1996 with the American Type Culture Collection under accession number ATCC 98145, from which each clone comprising a particular polynucleotide is obtainable. Each clone has been transfected into separate bacterial cells (*E. coli*) in this composite deposit. Each clone can be removed from the vector in which it was deposited by performing an EcoRI/NotI digestion (5' cite, EcoRI; 3' cite, NotI) to produce the appropriately sized fragment for such clone (approximate clone size fragment are identified below). Bacterial cells containing a particular clone can be obtained from the composite deposit as follows:

An oligonucleotide probe or probes should be designed to the sequence that is known for that particular clone. This sequence can be derived from the sequences provided herein, or from a combination of those sequences. The sequence of the oligonucleotide probe that was used to isolate each full-length clone is identified below, and should be most reliable in isolating the clone of interest.

| <u>Clone</u> | <u>Probe Sequence</u> |
|--------------|-----------------------|
| AY421_2 | SEQ ID NO:29 |
| BV278_2 | SEQ ID NO:30 |
| 25 C544_1 | SEQ ID NO:31 |
| CC332_33 | SEQ ID NO:32 |
| CC365_40 | SEQ ID NO:33 |
| CG68_4 | SEQ ID NO:34 |
| D329_1 | SEQ ID NO:35 |
| 30 H698_3 | SEQ ID NO:36 |
| H963_20 | SEQ ID NO:37 |

In the sequences listed above which include an N at position 2, that position is occupied in preferred probes/primers by a biotinylated phosphoramidite residue rather than a nucleotide (such as , for example, that produced by use of biotin phosphoramidite (1-dimethoxytrityloxy-

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2-(N-biotinyl-4-aminobutyl)-propyl-3-O-(2-cyanoethyl)-(N,N-diisopropyl)-phosphoramadite)
(Glen Research, cat. no. 10-1953)).

The design of the oligonucleotide probe should preferably follow these parameters:

- 5 (a) It should be designed to an area of the sequence which has the fewest
 ambiguous bases ("N's"), if any;
- (b) It should be designed to have a T_m of approx. 80 ° C (assuming 2° for each A
 or T and 4 degrees for each G or C).

10 The oligonucleotide should preferably be labeled with γ - ^{32}P ATP (specific activity 6000
Ci/mmole) and T4 polynucleotide kinase using commonly employed techniques for labeling
oligonucleotides. Other labeling techniques can also be used. Unincorporated label should
preferably be removed by gel filtration chromatography or other established methods. The
amount of radioactivity incorporated into the probe should be quantitated by measurement in
a scintillation counter. Preferably, specific activity of the resulting probe should be
15 approximately $4\text{e}+6$ dpm/pmole.

 The bacterial culture containing the pool of full-length clones should preferably be
thawed and 100 μl of the stock used to inoculate a sterile culture flask containing 25 ml of
sterile L-broth containing ampicillin at 100 $\mu\text{g}/\text{ml}$. The culture should preferably be grown to
saturation at 37°C, and the saturated culture should preferably be diluted in fresh L-broth.
20 Aliquots of these dilutions should preferably be plated to determine the dilution and volume
which will yield approximately 5000 distinct and well-separated colonies on solid
bacteriological media containing L-broth containing ampicillin at 100 $\mu\text{g}/\text{ml}$ and agar at 1.5%
in a 150 mm petri dish when grown overnight at 37°C. Other known methods of obtaining
distinct, well-separated colonies can also be employed.

25 Standard colony hybridization procedures should then be used to transfer the colonies
to nitrocellulose filters and lyse, denature and bake them.

 The filter is then preferably incubated at 65°C for 1 hour with gentle agitation in 6X
SSC (20X stock is 175.3 g NaCl/liter, 88.2 g Na citrate/liter, adjusted to pH 7.0 with NaOH)
containing 0.5% SDS, 100 $\mu\text{g}/\text{ml}$ of yeast RNA, and 10 mM EDTA (approximately 10 mL per
30 150 mm filter). Preferably, the probe is then added to the hybridization mix at a concentration
greater than or equal to $1\text{e}+6$ dpm/mL. The filter is then preferably incubated at 65°C with
gentle agitation overnight. The filter is then preferably washed in 500 mL of 2X SSC/0.5%
SDS at room temperature without agitation, preferably followed by 500 mL of 2X SSC/0.1%
SDS at room temperature with gentle shaking for 15 minutes. A third wash with 0.1X
35 SSC/0.5% SDS at 65°C for 30 minutes to 1 hour is optional. The filter is then preferably dried

and subjected to autoradiography for sufficient time to visualize the positives on the X-ray film. Other known hybridization methods can also be employed.

The positive colonies are picked, grown in culture, and plasmid DNA isolated using standard procedures. The clones can then be verified by restriction analysis, hybridization
5 analysis, or DNA sequencing.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, *et al.*, *Bio/Technology* 10, 773-778 (1992) and in R.S. McDowell, *et al.*, *J.*
10 *Amer. Chem. Soc.* 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion
15 of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by
20 translation of the nucleotide sequence of each disclosed clone. The mature form of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with ATCC) in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein may also be determinable from the amino acid sequence of the full-length form.

25 The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials.

30 Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques
35 for determination of such domains from sequence information.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

5 The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

10 The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, Nucleic Acids Res. 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" means that the
15 isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

20 A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

25 Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria,
30 it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

35 The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell

expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing
5 a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The
10 purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

15 Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and InVitrogen, respectively.
20 The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl
25 or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

30 The protein of the invention may also be expressed as a product of transgenic animals, *e.g.*, as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known
35 to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing

primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

Research Uses and Utilities

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage

of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the
5 feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

10 Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor
15 dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

20 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter
25 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bertagnolli et al., *J. Immunol.* 145:1706-1712, 1990; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Bertagnolli, et al., *J. Immunol.* 149:3778-3783, 1992; Bowman et al., *J. Immunol.* 152: 1756-1761, 1994.

30 Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: *Polyclonal T cell stimulation*, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and *Measurement of mouse and human Interferon γ* , Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a.
35 Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

- Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto.
- 5 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett,
- 10 F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.
- 15 Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3,
- 20 In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

25 Immune Stimulating or Suppressing Activity

- A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down)
- 30 growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including
- 35 infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, *Leishmania* spp., malaria

spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention
5 include, for example, connective tissue disease, multiple sclerosis, systemic lupus
erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre
syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis,
graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the
present invention may also to be useful in the treatment of allergic reactions and conditions,
10 such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions,
in which immune suppression is desired (including, for example, organ transplantation), may
also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a
number of ways. Down regulation may be in the form of inhibiting or blocking an immune
15 response already in progress or may involve preventing the induction of an immune response.
The functions of activated T cells may be inhibited by suppressing T cell responses or by
inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is
generally an active, non-antigen-specific, process which requires continuous exposure of the
T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or
20 anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-
specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance
can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the
absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without
25 limitation B lymphocyte antigen functions (such as , for example, B7)), *e.g.*, preventing high
level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and
organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T
cell function should result in reduced tissue destruction in tissue transplantation. Typically,
in tissue transplants, rejection of the transplant is initiated through its recognition as foreign
30 by T cells, followed by an immune reaction that destroys the transplant. The administration
of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural
ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2
activity alone or in conjunction with a monomeric form of a peptide having an activity of
another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation
35 can lead to the binding of the molecule to the natural ligand(s) on the immune cells without

transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting

an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

5 Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate
10 infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

 In another application, up regulation or enhancement of antigen function (preferably
15 B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from
20 a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

25 The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be
30 transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-
35 3) induces a T cell mediated immune response against the transfected tumor cell. Optionally,

a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated
5 immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation,
10 those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, *Immunologic studies in Humans*); Herrmann et al., *Proc. Natl. Acad. Sci. USA* 78:2488-2492, 1981; Herrmann et al., *J. Immunol.* 128:1968-1974, 1982; Handa et al., *J. Immunol.*
15 135:1564-1572, 1985; Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Herrmann et al., *Proc. Natl. Acad. Sci. USA* 78:2488-2492, 1981; Herrmann et al., *J. Immunol.* 128:1968-1974, 1982; Handa et al., *J. Immunol.* 135:1564-1572, 1985; Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bowman et al., *J. Virology* 61:1992-1998; Takai et al., *J. Immunol.* 140:508-512, 1988; Bertagnolli et al.,
20 *Cellular Immunology* 133:327-341, 1991; Brown et al., *J. Immunol.* 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. *Immunol.* 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production,
25 Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H.
30 Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, *Immunologic studies in Humans*); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Bertagnolli et al., *J. Immunol.* 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed
35 by dendritic cells that activate naive T-cells) include, without limitation, those described in:

Guery et al., *J. Immunol.* 134:536-544, 1995; Inaba et al., *Journal of Experimental Medicine* 173:549-559, 1991; Macatonia et al., *Journal of Immunology* 154:5071-5079, 1995; Porgador et al., *Journal of Experimental Medicine* 182:255-260, 1995; Nair et al., *Journal of Virology* 67:4062-4069, 1993; Huang et al., *Science* 264:961-965, 1994; Macatonia et al., *Journal of*
 5 *Experimental Medicine* 169:1255-1264, 1989; Bhardwaj et al., *Journal of Clinical Investigation* 94:797-807, 1994; and Inaba et al., *Journal of Experimental Medicine* 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte
 10 homeostasis) include, without limitation, those described in: Darzynkiewicz et al., *Cytometry* 13:795-808, 1992; Gorczyca et al., *Leukemia* 7:659-670, 1993; Gorczyca et al., *Cancer Research* 53:1945-1951, 1993; Itoh et al., *Cell* 66:233-243, 1991; Zacharchuk, *Journal of Immunology* 145:4037-4045, 1990; Zamai et al., *Cytometry* 14:891-897, 1993; Gorczyca et al., *International Journal of Oncology* 1:639-648, 1992.

15 Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., *Blood* 84:111-117, 1994; Fine et al., *Cellular Immunology* 155:111-122, 1994; Galy et al., *Blood* 85:2770-2778, 1995; Toki et al., *Proc. Nat. Acad Sci. USA* 88:7548-7551, 1991.

20 Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of
 25 erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with
 30 chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-
 35 mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell

disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation
5 (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

10 Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others,
15 proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of*
20 *Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of*
25 *Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth Activity

30 A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone
35 fractures and cartilage damage or defects in humans and other animals. Such a preparation

employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. *De novo* tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically,

a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be
5 treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-
10 healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular
15 (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration
20 and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

25 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No.
30 WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

35

Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- β group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be

readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

- 5 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, 10 A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

15

Hemostatic and Thrombolytic Activity

- A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other 20 hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

- 25 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

30

Receptor/Ligand Activity

- A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases 35 and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell

interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by
5 inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

10

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing
15 or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or
20 elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages
25 other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another
30 material or entity which is cross-reactive with such protein.

ADMINISTRATION AND DOSING

A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical
35 composition when combined with a pharmaceutically acceptable carrier. Such a composition

may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as

micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The

tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μ g to about 100 mg (preferably about 0.1 μ g to about 10 mg, more preferably about 0.1 μ g to about 1 mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range

of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal
5 and monoclonal antibodies which specifically react with the protein. Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem.Soc. 85,
10 2149-2154 (1963); J.L. Krstenansky, *et al.*, FEBS Lett. 211, 10 (1987). Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In
15 the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition
20 topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful
25 agents other than a protein of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage,
30 providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular
35 application of the compositions will define the appropriate formulation. Potential matrices for

the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Jacobs, Kenneth
McCoy, John
LaVallie, Edward
Racie, Lisa
Merberg, David
Treacy, Maurice
Spaulding, Vikki
- (ii) TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM
- (iii) NUMBER OF SEQUENCES: 37
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Genetics Institute, Inc.
 - (B) STREET: 87 CambridgePark Drive
 - (C) CITY: Cambridge
 - (D) STATE: Massachusetts
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Brown, Scott A.
 - (B) REGISTRATION NUMBER: 32,724
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 498-8224
 - (B) TELEFAX: (617) 876-5851

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 949 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | |
|---|-----|
| AGANACCACA TATCCCTGGG TTGTGGAAGA NGTGGCTGTC CCCTGTCATC AGTNTNCANC | 60 |
| GATTGCTCTT TCCGCCGTNG ANGGCCTTGA NNGGGAGGCA CTATCTGCCG CTCCTGGCTC | 120 |
| CTACGGCANC NCCTAGAGCA CANTNTGNTT GCNTCATGCN CCCTTTGAGG CCANGGNAAT | 180 |
| ACACCACCAT CTCTGAAGTA ACTTTGNAAT CTGGAAGGGG TACANTGTCC CTTCCCTCAA | 240 |
| AGGCTGCTGA RCGGGTGGTG GGCCGATRGC TCCTGGTCTG CASTGRAACA GTGGCTGGAG | 300 |
| CASTTATTCT TGGTGGGAGT AACTAKGTTG ACAGAGTCTG GCCTCTCGAT GGTAGATTGG | 360 |
| CATTTAATAA AGGARATGAA GCCMCCTACM AGCCACMKAG GAATGGGAAG CARAATTCCA | 420 |
| AAGATACCAG CAATTTCCAG AATTTAAAAT CTTGAATCGT GATATGACAC TGACAGAATT | 480 |
| CAAGTTCATC TGGTACATGG AGTACTCACA CCGAATGTGG GGTGCGCTTG TAGGCCTTGT | 540 |
| GAACATCCTG CCTGCTGCCT ACTTTTGGAG AAAGGGCTGG CTCAGCCGTG GCATGAAAGG | 600 |
| ACGTGTTCTT GCCCTCTGTG GCCTCGTCTG CTTCCAGGGT CTGTTGGGAT GGTATATGGT | 660 |
| GAAAAGTGGA CTAGAAGAAA AATCAGACTC CCATGACATC CCTCGGGTCA GTCAGTACCG | 720 |
| CCTTGCTGCC CACCTGGGAT CAGCCCTGGT TCTTTATTGT GCCAGCTTGT GGACCTCACT | 780 |
| GTCAGTGCTA CTCCCTCCGC ACAAGTTGCC TGAAACCCAC CAACTCCTAC AGTTGAGACG | 840 |
| ATTTGCTCAT GGAACAGCAG GTCTGGTGTT CCTTACGGCC CTCTCAGGGG CTTTGTGGC | 900 |
| AGGGCTAGAT GCTGGGCTTG TTTATAACTC CTTTCCCAA ATGGGAGAA | 949 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Gly Arg Val Leu Ala Leu Cys Gly Leu Val Cys Phe Gln Gly

1 5 10 15
 Leu Leu Gly Trp Tyr Met Val Lys Ser Gly Leu Glu Glu Lys Ser Asp
 20 25 30
 Ser His Asp Ile Pro Arg Val Ser Gln Tyr Arg Leu Ala Ala His Leu
 35 40 45
 Gly Ser Ala Leu Val Leu Tyr Cys Ala Ser Leu Trp Thr Ser Leu Ser
 50 55 60
 Leu Leu Leu Pro Pro His Lys Leu Pro Glu Thr His Gln Leu Leu Gln
 65 70 75 80
 Leu Arg Arg Phe Ala His Gly Thr Ala Gly Leu Val Phe Leu Thr Ala
 85 90 95
 Leu Ser Gly Ala Phe Val Ala Gly Leu Asp Ala Gly Leu Val Tyr Asn
 100 105 110
 Ser Phe Pro Lys Met Gly Glu
 115

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 117 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 60
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAA 117

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

TAGGCCATGA AGGCCGGCCT TCATGGCCTA AAATGTTCAA GAACAACACA TTGATATGTG      60
GAAATATTCT ATAAGGTTTT CTTTTGTTCC CTTANAATTC ATTGGAGGGA TGCAGTAAAA      120
ACTGTAGTAG AAACCTTGAA ACACCCATAT GTGAAAAGGT CTGTGGAAAT TGAGGCCTCT      180
ACATTAAAAG TGCAGAACAA CTGTTTTTACA GTCAAAGTGC TAGGAAACCT GATANGATAC      240
TTCCCTTTGG CACAAAAACA CCCTGGGTGC TACATACAGG GANCATGACC TTTGGTGAAT      300
ATGTGGCACT AATTTTTTTT ACCTTAATCA TATTCTTGTC AAGTAGGCAA CCC              353

```

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 498 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

GTAAGTGAAG GCNTAAAGAA AGTAACCCAG GGAGTCCCGG TCCCAGTTTT AATATTTGTG      60
GATTTGTTGT CACACACATT GTTTAGTCCT GAAACTAAAA CCTATTTTAT AAATAGTAGG      120
GTTAATTTCC TCGAAACAAT TTTCTTTATT AATAAATGTC CTGTGGGTTT AGAAATATCA      180
GGTAAATATT TGAATACAGA ATGATGATTG CAATTACTGT TACAAGCGTG AAACACAAAC      240
TTCAGATCAA ATCTAGAGTT GCTTGATTTA ATGCATGCTA GCAACAGCCT TAACTTTGGA      300
TTCAGTTATT TGAAACACTT TTCCGGCATC TTTCCCTTTC TAATGTTGTG GGGTGGAAAC      360
CGGATGGCAA ATCACTGTGA GCCGGATACC TCAGCACAGT CCACCTTGTG TGTGACTTCA      420
CAAATGGGGG ACTTCACAAA TGGGGTAACT GAATGTTATT ACTTTCAAAT TTTGACATGG      480
AGCATTATGA TCAAGGAA

```

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 76 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met His Ala Ser Asn Ser Leu Asn Phe Gly Phe Ser Tyr Leu Lys His
1 5 10 15

Phe Ser Gly Ile Phe Pro Phe Leu Met Leu Trp Gly Gly Asn Arg Met
20 25 30

Ala Asn His Cys Glu Pro Asp Thr Ser Ala Gln Ser Thr Leu Cys Val
35 40 45

Thr Ser Gln Met Gly Asp Phe Thr Asn Gly Val Thr Glu Cys Tyr Tyr
50 55 60

Phe Gln Ile Leu Thr Trp Ser Ile Met Ile Lys Glu
65 70 75

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | | | | | | |
|-------|-------|-------|-------|-------|-------|----|
| AAAAA | AAAAA | AAAAA | AAAAA | AAAAA | AAAAA | 60 |
| AAAAA | | | | | | 69 |

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CAGAGACAGA CAACTGGTAC CTCTCCCTGC AGCTCATGTG CCCTGAGAAT GCTGAGGACT 60
 GTGAGCAGGC TGTGGTCCAC GTGGAGACCA CCTTGTACCT GGTGCCCTGT TTGAACGATT 120
 GTGGACCCTA TGGCCAGTGC CTCCTGCTCC GCAGACACAG CTACCTGTAT GCCAGCTGCA 180
 GCTGCAAGGC AGGCTGGCGT GGGTGGAGCT GCACGGACAA CAGCACAGCC CAGACGGTGG 240
 CCCAGCAGAG GGC GGCCACA CTGCTGCTCA CGCTCAGCAA CCTCATGTTC CTGGCCCCCA 300
 TCGCCGTCTC AGTGC GGCGA TTCTTCCTGG TGGAGTCGAC CGTCTACGCC TACACCATGT 360
 TCTTCTCCAC GTTCTACCAC GCCTGCGACC AGCCCGGGGA GGCGGTGCTG TGCATCCTCA 420
 GCTACGACAC GCTGCAGTAC TGC GACTTCT TGGGCTCCGG GGCGGCCATC TGGGTACCA 480
 TCCTGTGCAT GGCACGGCTC AAGACAGTCC TGAAATACGT GCTGTTTCTT CTGGGTACAC 540
 TGGTCATCGC CATGTCCTTG CAGCTGGACC GCAGGGGCAT GTGGAACATG CTGGGGCCCT 600
 GCCTCTTTGC CTTGCTGATC ATGGCCTCCA TGTGGGCTTA CCGCTGCGGG CACCGGCGCC 660
 AGTGCTACCC CACCTCGTGG CAGCGCTGGG CTTTCTACCT CCTGCCCCGC GTCTCTACGG 720
 CC 722

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Cys Pro Glu Asn Ala Glu Asp Cys Glu Gln Ala Val Val His Val
 1 5 10 15
 Glu Thr Thr Leu Tyr Leu Val Pro Cys Leu Asn Asp Cys Gly Pro Tyr
 20 25 30
 Gly Gln Cys Leu Leu Leu Arg Arg His Ser Tyr Leu Tyr Ala Ser Cys
 35 40 45
 Ser Cys Lys Ala Gly Trp Arg Gly Trp Ser Cys Thr Asp Asn Ser Thr
 50 55 60
 Ala Gln Thr Val Ala Gln Gln Arg Ala Ala Thr Leu Leu Leu Thr Leu
 65 70 75 80

Ser Asn Leu Met Phe Leu Ala Pro Ile Ala Val Ser Val Arg Arg Phe
 85 90 95
 Phe Leu Val Glu Ser Thr Val Tyr Ala Tyr Thr Met Phe Phe Ser Thr
 100 105 110
 Phe Tyr His Ala Cys Asp Gln Pro Gly Glu Ala Val Leu Cys Ile Leu
 115 120 125
 Ser Tyr Asp Thr Leu Gln Tyr Cys Asp Phe Leu Gly Ser Gly Ala Ala
 130 135 140
 Ile Trp Val Thr Ile Leu Cys Met Ala Arg Leu Lys Thr Val Leu Lys
 145 150 155 160
 Tyr Val Leu Phe Leu Leu Gly Thr Leu Val Ile Ala Met Ser Leu Gln
 165 170 175
 Leu Asp Arg Arg Gly Met Trp Asn Met Leu Gly Pro Cys Leu Phe Ala
 180 185 190
 Phe Val Ile Met Ala Ser Met Trp Ala Tyr Arg Cys Gly His Arg Arg
 195 200 205
 Gln Cys Tyr Pro Thr Ser Trp Gln Arg Trp Ala Phe Tyr Leu Leu Pro
 210 215 220
 Gly Val Ser Thr Ala
 225

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ACTTACTAAC AACCCACAGC ATTCTTGGCA ACATCCTGCT GGCCGGGAGC GCAGCCTTGT 60
 TGCTGCCGCC ACCTGACCAG CCCGCCGAGC CCTGGGGCCT GTTCGCAGAA ATTCCCCTGC 120
 CACTATCAGA TCTGCAAGAA CGATCGGGAG GAACTGTACG CAGTGACGTG AACTGGCCT 180
 GGGGACAGCT GCTGCTCTGA TGACTCTTCA GCCAGAGCTG TATCGAGGGG AGGCGCTGTC 240
 CAGCCTTGGA CAGATTGATT TCCAGCTGAT AATGGCCTAG ATACCTCAA AAAAAAAAAA 300

AAAAAAAAAA

310

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

| | |
|---|-----|
| CGAACTTGGT CGGGGCGCGG ATCCCGAGAG GGAAAGTCTT TAACAACCGC ACGAGGGAGT | 60 |
| TCGACTGGCG AACTGGAAGG CCACGCCTCC TCCCGCCTGC CCCCTCAGCC CTGTGGNTGG | 120 |
| GGGCAGAGCT CAGACTGTCT TCTGAAGATT GATGTCATT TCCTTGAGCT CTTTAATTTT | 180 |
| GTTGCCAATT TGGATAAACA TGGCACAAAT CCACCAGGGA GGTCCATATG AAAAAGAAAA | 240 |
| GACTACCGCC CTGAAAGATT TATTATCTAC GATATATTG GATGAACTAA TGAAAAAGA | 300 |
| TGAACCGCCT CTTGATTTTC CTGATACCCT GGAAAGAT | 338 |

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

| | |
|--|-----|
| AATTAAATTA AATTAAAATC TTTGTTACAA ACTATGAAAA TGAATATAAG TAAATTTTCAT | 60 |
| ATCATTTCTT TTCTAGATTT ATTATCTAGG ATAGATTTGG ATGAACTAAT GAAAAAGAT | 120 |
| GAACCGCCTC TTGATTTTCC TGATACCCTG GAAGGATTTG AATATGCTTT TAATGAAAAG | 180 |
| GGACAGTTAA GACACATAAA AACTGGGGAA CCATTTGTTT TTAACCTACCG GGAAGATTTA | 240 |
| CACAGATGG | 249 |

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

Met Lys Met Asn Ile Ser Lys Phe His Ile Ile Ser Phe Leu Asp Leu
1           5           10           15
Leu Ser Arg Ile Asp Leu Asp Glu Leu Met Lys Lys Asp Glu Pro Pro
20           25           30
Leu Asp Phe Pro Asp Thr Leu Glu Gly Phe Glu Tyr Ala Phe Asn Glu
35           40           45
Lys Gly Gln Leu Arg His Ile Lys Thr Gly Glu Pro Phe Val Phe Asn
50           55           60
Tyr Arg Glu Asp Leu His Arg Trp
65           70

```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

TTTCNTCAAA CAGGTTTTTA GGAGAGTGGG GATTTAAAGT CAGGATGTGG CCTTTTATT      60
TTAATTATAN ACTTAATTCT TAGAACAAGT AGAATGGGAA AGGAGTGA CT GATAAATCTA      120
AGATTCAAAA TAGTCCCGTC GAAACTTAAA GGCCAGATTA TTGCTTTGGA GCTTTCTATA      180
GGTACTAGCC ATCCCGTCGT TAAATGTTTT CATGGATATT TGAAAAGAAG ACCATGTACC      240
TTTAATAACT GTTCTTTTCT NGAGTTTCTG CCTCGTGCTT TGACCTGGAT TGCATTATTA      300
TTGTTTATGC GAAGTAAAAA AAAAAAAAAA AA                                     332

```


(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 436 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

GCTTTTTTTT CCACNGGTGT CCACTCCCAG GTCCAANTGC AGATTTNGAA TTCGGCTTTC      60
ATGGCCTAGC AGTTAGGAAA GTARCGTTAT GAGTTGWACT GAAAATGTTG ATTCTMTAAT      120
CTGCCAGAAA AGGAMCTGTC TTTTCATGCA GATTTTCATAT TGTCTTTGTC CTTTTTCATTG      180
CTTCTTGACC TTCCTGGCAG GTGTCGCTCA GTTTCTTCCT GTTTCCTTC CTGTCCTCTC      240
CACACCTGCT ATCCCGTCCC ACTCCCATCT ACCTCCCGGG AAGCCAGCCC TGCATGCTGA      300
GTTTGTGACC TGCTTCATTG CCATTTTCATT TCTAGAGGGT TTAGAGGTGA CCTGGAACCG      360
TTCCCTTTCC CTCTCCTACC CCCTCCTCTG CAACACCAAG AGGCCTGGAG GGGCAGACAG      420
AAAGCAGCCA GCCACG                                     436

```

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 116 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Met Ser Xaa Thr Glu Asn Val Asp Ser Xaa Ile Cys Gln Lys Arg Xaa
1           5           10           15
Cys Leu Phe Met Gln Ile Ser Tyr Cys Leu Cys Pro Phe His Cys Phe
                20           25           30
Leu Thr Phe Leu Ala Gly Val Ala Gln Phe Leu Pro Val Ser Leu Pro
35           40           45

```

Val Leu Ser Thr Pro Ala Ile Pro Ser His Ser His Leu Pro Pro Gly
 50 55 60

Lys Pro Ala Leu His Ala Glu Phe Val Thr Cys Phe Ile Pro Ile Ser
 65 70 75 80

Phe Leu Glu Gly Leu Glu Val Thr Trp Asn Arg Ser Leu Ser Leu Ser
 85 90 95

Tyr Pro Leu Leu Cys Asn Thr Lys Arg Pro Gly Gly Ala Asp Arg Lys
 100 105 110

Gln Pro Ala Thr
 115

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTATTTTCT GGGGATAGAG GGGGTGGGGT TAGGGATNTC CCTGTAGATT AGTTCAGAA 60

TGGGGTGTCT GTATATACTG TATTAATAGG CATGTTTGAN TTTCGTAAAG GGACGTTAGT 120

AGCTGCTGCA GNTCCTGTTT GGAAACCCCA TGAACAATTC CCAGTTTTTT GTAAGTGTC 180

GTGCGAGANA CATTTGANTC TTGTGTTTGT ATCTCCTTTT NATGATTGCT NNACCNACCC 240

ATNTNTTTTN GGGGAGGGGT GAAAAGAGAT TTGAAATAAA AATGTTTAGA AATTAAAAAA 300

AAACAAAAAA AAAAAAAA 318

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1055 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```

GTTAGACACA GGACCTGCTG GGCCACANAA AGGAGGCTCT GGGTAGACNC ACTANATTAC      60
TGGATAAATC ACTTCAATTT CCCAATGAAT TTTATATTGT TTATTTTAT ACCTGGAGTT      120
TTTTCCTTAA AAAGTACACT TTGAANCCTA CTATTGAAGC ATTGCCTAAT GTGCTACCTT      180
TAAATGAAGA TGTTAATAAG CAGGAAGAAA AGAATGAAGA TCATACTCCC AATTATGCTC      240
CTGNTAANGA GAAAAATGGC AATTATTATA AAGATATAAA ACAATATGTG TTCACAACAC      300
AAAATCCAAA TGGCACTGAG TNTGAAATAT TTGTGAGAGC CACAAC TGAC CTGAATTTTG      360
NTTTAAAAAA CGATAAACT GTCAATGCAA NTACATATGA AAAATCCACC ATTGAAGAAG      420
AAACAANTAN TAGCGAACCC TCTCATAAAA ATATTCAAAG ATCAACCCCA AACGTGCCTG      480
CAATTTGGAC AATGTTAGCT AAAGCTATAA ATGGAACAGC AGTGGTCATG GATGATAAAG      540
ATCAATTATT TCACCCAATT CCAGAGTCTG ATGTGAATGC TACACAGGGA GAAAATCAGC      600
CAGATCTAGA GGATCTGAAG ATCAAAATAA TGCTGGGAAT CTCGTTGAAG ACCCTCCTCC      660
TCTTTGTGGT CCTTCTTGGC ATTCTGTAGT GCTACACTGT ACAAAC TGAG GCATCTGAGT      720
TATAAAAGTT GTGAGAGTCA GTACTCTGTC AACCCAGAGC TGGCCACGAT GTCTTACTTT      780
CATCCATCAG AAGGTGTTTC AGATACATCC TTTTCCAAGA GTGCAGAGAG CAGCACATTT      840
TTGGGTACCA CTTCTTCAGA TATGAGAAGA TCAGGCACAA GAACATCAGA ATCTAAGATA      900
ATGACGGATA TCATTTCCAT AGGCTCAGAT AATGAGATGC ATGAAAACGA TGAGTCGGTT      960
ACCCGGTGAA GAAATCAAGG AACCCGGTGA AGAAATCTTA TTGATGAATA AATAACTTTA     1020
ATTATTTTGT CATCAAAAAA AAAAAAAAAA AAAAAA                                1055

```

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

Met Ser Tyr Phe His Pro Ser Glu Gly Val Ser Asp Thr Ser Phe Ser
1           5           10           15

```

Lys Ser Ala Glu Ser Ser Thr Phe Leu Gly Thr Thr Ser Ser Asp Met
 20 25 30
 Arg Arg Ser Gly Thr Arg Thr Ser Glu Ser Lys Ile Met Thr Asp Ile
 35 40 45
 Ile Ser Ile Gly Ser Asp Asn Glu Met His Glu Asn Asp Glu Ser Val
 50 55 60
 Thr Arg
 65

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

| | |
|--|-----|
| GACTGCGTCC TCATCCCCAG CAAACCTTGG CCCGGAGATG CTTCCCCGCT ATCCACGCCT | 60 |
| ACAAGGGTGT CCTGATGGTG GGCAATGAGA CGACCTATGA GGATGGGCAT GGCTCCCGGA | 120 |
| AAAACATCAC AGACCTGGTG GAAGGCGCCA AGAAAGCCAA TGGAGTCCTA GAGGCGCGGC | 180 |
| AACTCGCCAT GCGCATATTT GAAGATTACA CCGTCTCTTG GTACTGGATT ATCATAGGCC | 240 |
| TGGTCATTGC CATGGCGATG AGCCTCCTGT TCATCATCCT GCTTCGCTTC CTGGCTGGTA | 300 |
| TTATGGTCTG GGTGAATGAT CATCATGGTG ATTCTGGTGC TGGGCTACGG AATATTTTAC | 360 |
| TGCTACATGG AGTTACTCCC GACTGCGTGG TGAGGCGGTC TGATGTCTCT TTGGTGGACT | 420 |
| CGGCTTTCAG ACGGATTCCG GGTGTACTGC ACTTACGGCA GACTGGTTGG CCTTTAGTGA | 480 |
| GTCACAGTCT CCCATTCCCTG CCCCCACATG AGGCCTTGGA GGGAGTGGGG AGCCCAGCCG | 540 |
| GCTCAGCCTT TGCCCTTTGC AGTGATCATT CTGAGTATCC TTGAAGTCAT TATCCAAAAA | 600 |
| AAAAAAAAAG GCCCCTGCCC ATTTACTGCG AAAACCTGCA ACCCAGAGAC CTTCCCCTCC | 660 |
| TCCAATGAGT CCCGCCAATG CCCCAATGCC CGTTGCCAGT TCGCCTTCTA CGGTGGTGAG | 720 |
| TCGGGCTACC ACCGGGCCCT GCTGGGCCTG CAGATCTTCA ATGCCTTCAT GTTCTTCTGG | 780 |
| TTGGCCCAAC TTCGTGCTGG CGCTGGGCCA AGGTCAACGC TGGCCGGGGC CTTTGCTTCC | 840 |

```

TAATTAAGTGG GGCCTGCGC AAGCCGGACG ACCTGCCGGC CTTCCCGTTC TTCTTCTGCC   900
TTTGGCCGGG CGCTCAGGTA CCACACAGGC TCCCTGGCCT TTGGCGCGCT CATCCTGGCC   960
ATTGTGCAGA TCATCCGTGT GATACTCGAG TACCTGGATC AGCGGCTGAA AGCTGCAGAG  1020
AACAAGTTTG CCAAGTGCCT CATGACCTGT CTCAAATGCT GCTTCTGGTG CCTGGAGAAG  1080
TTCATCAAAT TCCTTAATAG GAATGCCTAC ATCATGATTG CCATCTACGG CACCAATTTTC  1140
TGCACCTCGG CCAGGAATGC CTTCTTCCTG CTCATGAGAA ACATCATCAG AGTGGCTGTC  1200
CTGGATAAAG TTAGTGACTT CCTCTTCCTG TTGGGCAAAC TTCTGATCGT TGGTAGTGTC  1260
GGGATCCTGG CTTTCTTCTT CTTACCCAC CGTATCAGGA TCGTGCAGGA TACAGCACCA  1320
CCCCTCAATT ATTACTGGGT TCCTATACTG ACGGTGATCG TTGGCTCCTA CTTGATTGCG  1380
TCGACGGCC                                     1389

```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

Met Thr Cys Leu Lys Cys Cys Phe Trp Cys Leu Glu Lys Phe Ile Lys
1           5           10           15
Phe Leu Asn Arg Asn Ala Tyr Ile Met Ile Ala Ile Tyr Gly Thr Asn
20          25          30
Phe Cys Thr Ser Ala Arg Asn Ala Phe Phe Leu Leu Met Arg Asn Ile
35          40          45
Ile Arg Val Ala Val Leu Asp Lys Val Thr Asp Phe Leu Phe Leu Leu
50          55          60
Gly Lys Leu Leu Ile Val Gly Ser Val Gly Ile Leu Ala Phe Phe Phe
65          70          75          80
Phe Thr His Arg Ile Arg Ile Val Gln Asp Thr Ala Pro Pro Leu Asn
85          90          95
Tyr Tyr Trp Val Pro Ile Leu Thr Val Ile Val Gly Ser Tyr Leu Ile
100         105         110

```

Ala Ser Thr Ala
115

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAAAAAAAAA AAAAAAAAAA ANAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 60
 AAAAAAAAAA 69

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 422 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TTTTTTTTTG CTCCAGCACC AGTGTTCCTT AAACACCTTA CCAGCAGCTT CCATTTTGGC 60
 ATGGAANAGT GTTCTCGGCA ATGGCCATTT GTCATCACTG GGAACCAGAG ACACCCATCC 120
 CTACGCCAGC TTGAGCCGTG CACTGCANAC ACAATGCTGT ATTTCTTCTC CCAGTCACCT 180
 GATGAGCCAG CAGTATAGAC CATATNGTTT CTTCACTAAA TTGACTGCAN ATGAGCTGTG 240
 GAAAGGCGCT TTAGCAGAGA CTGGTGCTGG AGCAAAAAA GGAAGAGGCC AAAGAACTAA 300
 AAAGAAGAAA AGAAAGGATC TGAACAGGGG TCANATCATT GGTGAAGGGC GTTNTGGTTT 360
 TCTATGGCCC GGACTGAATG TCCCTCCTTA TGAAAAATGG AGCAGTGCAG ACCATTGCCC 420
 CC 422

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 515 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
GCAACCACAA TGGGCAGAGG CAACATTCTT CCCGGATTTT CACAACATGG AGGCCCTTTC      60
TTATCAGCCA GCTGTTGATG GGTTTCCTGT CTGGAGAGCC CACGGAAGAG GCCCTGGGTG      120
AGGCTGAGCA TATTAATGGA CCCAGAGACC TTGGCATACA TGTCTTTGAT GCCAATGAGC      180
CGGCAGATGG TGATGATGGC CCTGTGGCAG CGGAGGCCGT AACCTTTGGG TTGTTTCTTC      240
ATCTTGATAT GCGTCCTTTT AAATCTTAAT GAAATATCAT GGAATATTGT ATGGTCTTCA      300
TATCGTTCTA TATAATGCAA ATGGTGAAC TCTCTGTTCT TTGCTTTCCT GAAAGCATCC      360
ATCCGATCAG TAGCTTTCCC AATAGAAAAA CCTGCAGCTC CTTTCCGTT CCCCACAGCC      420
ACCAAGACAC GGATCGATTT CTTTCTTCCC TCTTTCGAG TCATAGTGAA AACGTTTCTT      480
ACCTCAAGTA TCCTGGTATC AAAATCCTCA TATGT                                515
```

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 79 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
Met Glu Tyr Cys Met Val Phe Ile Ser Phe Tyr Ile Met Gln Met Val
1           5           10          15
Asn Cys Ser Val Leu Cys Phe Pro Glu Ser Ile His Pro Ile Ser Ser
20          25          30
Phe Pro Asn Arg Lys Thr Cys Ser Ser Phe Ser Val Pro His Ser His
35          40          45
```

Gln Asp Thr Asp Arg Phe Leu Ser Ser Leu Phe Arg Ser His Ser Glu
 50 55 60

Asn Val Ser Tyr Leu Lys Tyr Pro Gly Ile Lys Ile Leu Ile Cys
 65 70 75

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAAAAAAAA NNTNNTTTT TTAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 60
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 120
 AAAAAAAAAA AAAAAAAAAA AAAA 144

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1243 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGCTTCTCTG AAGACTTGCA GCAAGGCTTG CTGAGGCTCA CAGAAGATAG CCCAGTGTT 60
 TTGGAGTGGT TTTGAATGTG ATTCTGAGAT CAGACTGACT GAGCTGGAAT CCTGGCTTTA 120
 TATCTTACCA GCTACACAAC CTGGAGTCT TAGAAATTTT TTCTTTTCAA TAAGCAGTCA 180
 TCCTTACTTT CCCTCAAGAT GACAAACAGT TCGTTCTTCT GCCCAGTTTA TAAAGATCTG 240
 GAGCCATTCA CGTATTTTTT TTATTTAGTT TTCCTGTTG GAATTATTGG AAGTTGTTTT 300
 GCAACCTGGG CTTTATACA GAAGAATACG AATCACAGGT GTGTGAGCAT CTACTTAATT 360
 AATTGCTTA CAGCCGATTT CCTGCTTACT CTGGCATTAC CAGTGAAAAT TGTGTGTTGAC 420


```

TTGGGTGTGG CACCTTGGA GCTGAAGATA TTCCACTGCC AAGTAACAGC CTGCCTCATC   480
TATATCAATA TGTATTTATC AATTATCTTC TTAGCATTTG TCAGCATTGA CCGCTGTCTT   540
CAGCTGACAC ACAGCTGCAA GATCTACCGA ATACAAGAAC CCGGATTTGC CAAAATGATA   600
TCAACCGTTG TGTGGCTAAT GGTCCCTTCTT ATAATGGTGC CAAATATGAT GATTCCCATC   660
AAAGACATCA AGGAAAAGTC AAATGTGGGT TGTATGGAGT TTAAAAAGGA ATTTGGAAGA   720
AATTGGCATT TGCTGACAAA TTTCATATGT GTAGCAATAT TTTTAAATTT CTCAGCCATC   780
ATTTTAATAT CCAATTGCCT TGTAATTCGA CAGCTCTACA GAAACAAAGA TAATGAAAAT   840
TACCCAAATG TGAAAAAGGC TCTCATCAAC ATACTTTTAG TGACCACGGG CTACATCATA   900
TGCTTTGTTT CTTACCACAT TGTCCGAATC CCGTATACCC TCAGCCAGAC AGAAGTCATA   960
ACTGATTGCT CAACCAGGAT TTCACTCTTC AAAGCCAAAAG AGGCTACACT GCTCCTGGCT  1020
GTGTCGAACC TGTGCTTTGA TCCTATCCTG TACTATCACC TCTCAAAGC ATTCCGCTCA  1080
AAGGTCAC TGACTTTTGC CTCACCTAAA GAGACCAAGG CTCAGAAAGA AAAATTAAGA  1140
TGTGAAAATA ATGCATAAAA GACAGGATTT TTTGTGCTAC CAATTCTGGC CTTACTGGAC  1200
CATAAAGTTA ATTATAGCTT TGAAAGATAA AAAAAAAAAA AAA                      1243

```

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

Met Thr Asn Ser Ser Phe Phe Cys Pro Val Tyr Lys Asp Leu Glu Pro
1           5           10           15
Phe Thr Tyr Phe Phe Tyr Leu Val Phe Leu Val Gly Ile Ile Gly Ser
20           25           30
Cys Phe Ala Thr Trp Ala Phe Ile Gln Lys Asn Thr Asn His Arg Cys
35           40           45
Val Ser Ile Tyr Leu Ile Asn Leu Leu Thr Ala Asp Phe Leu Leu Thr
50           55           60

```

```

Leu Ala Leu Pro Val Lys Ile Val Val Asp Leu Gly Val Ala Pro Trp
65                               70                               75                               80

Lys Leu Lys Ile Phe His Cys Gln Val Thr Ala Cys Leu Ile Tyr Ile
                        85                               90                               95

Asn Met Tyr Leu Ser Ile Ile Phe Leu Ala Phe Val Ser Ile Asp Arg
                        100                               105                               110

Cys Leu Gln Leu Thr His Ser Cys Lys Ile Tyr Arg Ile Gln Glu Pro
                        115                               120                               125

Gly Phe Ala Lys Met Ile Ser Thr Val Val Trp Leu Met Val Leu Leu
130                               135                               140

Ile Met Val Pro Asn Met Met Ile Pro Ile Lys Asp Ile Lys Glu Lys
145                               150                               155                               160

Ser Asn Val Gly Cys Met Glu Phe Lys Lys Glu Phe Gly Arg Asn Trp
                        165                               170                               175

His Leu Leu Thr Asn Phe Ile Cys Val Ala Ile Phe Leu Asn Phe Ser
                        180                               185                               190

Ala Ile Ile Leu Ile Ser Asn Cys Leu Val Ile Arg Gln Leu Tyr Arg
                        195                               200                               205

Asn Lys Asp Asn Glu Asn Tyr Pro Asn Val Lys Lys Ala Leu Ile Asn
210                               215                               220

Ile Leu Leu Val Thr Thr Gly Tyr Ile Ile Cys Phe Val Pro Tyr His
225                               230                               235                               240

Ile Val Arg Ile Pro Tyr Thr Leu Ser Gln Thr Glu Val Ile Thr Asp
                        245                               250                               255

Cys Ser Thr Arg Ile Ser Leu Phe Lys Ala Lys Glu Ala Thr Leu Leu
                        260                               265                               270

Leu Ala Val Ser Asn Leu Cys Phe Asp Pro Ile Leu Tyr Tyr His Leu
275                               280                               285

Ser Lys Ala Phe Arg Ser Lys Val Thr Glu Thr Phe Ala Ser Pro Lys
290                               295                               300

Glu Thr Lys Ala Gln Lys Glu Lys Leu Arg Cys Glu Asn Asn Ala
305                               310                               315

```

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ANAACACGTC CTTTCATGCC ACGGCTGAG

29

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GNTGCTCCAT TTCCTTGATC ATAATGCTC

29

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ANAGGGTAGA ACGTGGAGAA GAACATGGTG T

31

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TNTGGTTCCA TCTGTGTAAA TCTTCCCGG

29

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GNCACAAACT CAGCATGCAG GGCTGGCTT

29

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ANTCACATCA GACTCTGGAA TTGGGTGAA

29

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GNNTAAAACT TGTTCTCTGC AGCTTTCAGC CG

32

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GNCATTATAT AGAACGATAT GAAGACCAT

29

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCTGACACAC AGCTGCAAGA TCTACC

26

What is claimed is:

1. A composition comprising an isolated polynucleotide selected from the group consisting of:
 - (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1;
 - (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 593 to nucleotide 949;
 - (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 650 to nucleotide 949;
 - (d) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AY421_2 deposited under accession number ATCC 98145;
 - (e) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AY421_2 deposited under accession number ATCC 98145;
 - (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AY421_2 deposited under accession number ATCC 98145;
 - (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AY421_2 deposited under accession number ATCC 98145;
 - (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2;
 - (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity;
 - (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above; and
 - (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above.
2. A composition of claim 1 wherein said polynucleotide is operably linked to an expression control sequence.
3. A host cell transformed with a composition of claim 2.
4. The host cell of claim 3, wherein said cell is a mammalian cell.
5. A process for producing a protein, which comprises:

- (a) growing a culture of the host cell of claim 3 in a suitable culture medium;
and
 - (b) purifying the protein from the culture
6. A protein produced according to the process of claim 5.
7. The protein of claim 6 comprising a mature protein.
8. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:2;
 - (b) fragments of the amino acid sequence of SEQ ID NO:2; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone AY421_2 deposited under accession number ATCC 98145;
- the protein being substantially free from other mammalian proteins.
9. The composition of claim 8, wherein said protein comprises the amino acid sequence of SEQ ID NO:2.
10. The composition of claim 8, further comprising a pharmaceutically acceptable carrier.
11. A method for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically effective amount of a composition of claim 10.
12. The gene corresponding to the cDNA sequence of SEQ ID NO:1 or SEQ ID NO:3.
13. A composition comprising an isolated polynucleotide selected from the group consisting of:
- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5;
 - (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 271 to nucleotide 498;

- (c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone BV278_2 deposited under accession number ATCC 98145;
- (d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone BV278_2 deposited under accession number ATCC 98145;
- (e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone BV278_2 deposited under accession number ATCC 98145;
- (f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone BV278_2 deposited under accession number ATCC 98145;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:6;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ; and
- (k) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(h).

14. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:6;
- (b) fragments of the amino acid sequence of SEQ ID NO:6; and
- (c) the amino acid sequence encoded by the cDNA insert of clone BV278_2 deposited under accession number ATCC 98145;

the protein being substantially free from other mammalian proteins.

15. The gene corresponding to the cDNA sequence of SEQ ID NO:5, SEQ ID NO:4 or SEQ ID NO:7 .

16. A composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:8;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:8 from nucleotide 36 to nucleotide 722;
- (c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone C544_1 deposited under accession number ATCC 98145;
- (d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone C544_1 deposited under accession number ATCC 98145;
- (e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone C544_1 deposited under accession number ATCC 98145;
- (f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone C544_1 deposited under accession number ATCC 98145;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:9;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:9 having biological activity;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above; and
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above .

17. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:9;
- (b) the amino acid sequence of SEQ ID NO:9 from amino acid 101 to amino acid 185;
- (c) fragments of the amino acid sequence of SEQ ID NO:9; and
- (d) the amino acid sequence encoded by the cDNA insert of clone C544_1 deposited under accession number ATCC 98145;

the protein being substantially free from other mammalian proteins. .

18. The gene corresponding to the cDNA sequence of SEQ ID NO:8 or SEQ ID NO:10.

19. A composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:12;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:12 from nucleotide 34 to nucleotide 249;
- (c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone CC332_33 deposited under accession number ATCC 98145;
- (d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone CC332_33 deposited under accession number ATCC 98145;
- (e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone CC332_33 deposited under accession number ATCC 98145;
- (f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone CC332_33 deposited under accession number ATCC 98145;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:13;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:13 having biological activity;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above; and
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above .

20. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:13;
- (b) fragments of the amino acid sequence of SEQ ID NO:13; and
- (c) the amino acid sequence encoded by the cDNA insert of clone CC332_33 deposited under accession number ATCC 98145;

the protein being substantially free from other mammalian proteins.

21. The gene corresponding to the cDNA sequence of SEQ ID NO:12, SEQ ID NO:11 or SEQ ID NO:14 .

22. A composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 89 to nucleotide 436;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 212 to nucleotide 436;

(d) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone CC365_40 deposited under accession number ATCC 98145;

(e) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone CC365_40 deposited under accession number ATCC 98145;

(f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone CC365_40 deposited under accession number ATCC 98145;

(g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone CC365_40 deposited under accession number ATCC 98145;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above; and

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above .

23. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:16;

(b) the amino acid sequence of SEQ ID NO:16 from amino acid 17 to amino acid 116;

(c) fragments of the amino acid sequence of SEQ ID NO:16; and

(d) the amino acid sequence encoded by the cDNA insert of clone CC365_40 deposited under accession number ATCC 98145;

the protein being substantially free from other mammalian proteins.

24. The gene corresponding to the cDNA sequence of SEQ ID NO:15 or SEQ ID NO:17.

25. A composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:18;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:18 from nucleotide 769 to nucleotide 966;
- (c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone CG68_4 deposited under accession number ATCC 98145;
- (d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone CG68_4 deposited under accession number ATCC 98145;
- (e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone CG68_4 deposited under accession number ATCC 98145;
- (f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone CG68_4 deposited under accession number ATCC 98145;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:19;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:19 having biological activity;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ; and
- (k) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(h).

26. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:19;
- (b) the amino acid sequence of SEQ ID NO:19 from amino acid 18 to amino acid 57;
- (c) fragments of the amino acid sequence of SEQ ID NO:19; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CG68_4 deposited under accession number ATCC 98145;

the protein being substantially free from other mammalian proteins.

27. The gene corresponding to the cDNA sequence of SEQ ID NO:18.
28. A composition comprising an isolated polynucleotide selected from the group consisting of:
- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:20;
 - (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:20 from nucleotide 1042 to nucleotide 1389;
 - (c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone D329_1 deposited under accession number ATCC 98145;
 - (d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone D329_1 deposited under accession number ATCC 98145;
 - (e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone D329_1 deposited under accession number ATCC 98145;
 - (f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone D329_1 deposited under accession number ATCC 98145;
 - (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:21;
 - (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:21 having biological activity;
 - (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above; and
 - (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above.
29. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:21;
 - (b) fragments of the amino acid sequence of SEQ ID NO:21; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone D329_1 deposited under accession number ATCC 98145;
- the protein being substantially free from other mammalian proteins.
30. The gene corresponding to the cDNA sequence of SEQ ID NO:20 or SEQ ID NO:22.

31. A composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:24;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:24 from nucleotide 279 to nucleotide 515;
- (c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone H698_3 deposited under accession number ATCC 98145;
- (d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone H698_3 deposited under accession number ATCC 98145;
- (e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone H698_3 deposited under accession number ATCC 98145;
- (f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone H698_3 deposited under accession number ATCC 98145;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:25;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:25 having biological activity;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above; and
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above.

32. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:25;
 - (b) fragments of the amino acid sequence of SEQ ID NO:25; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone H698_3 deposited under accession number ATCC 98145;
- the protein being substantially free from other mammalian proteins.

33. The gene corresponding to the cDNA sequence of SEQ ID NO:24, SEQ ID NO:23 or SEQ ID NO:26.

34. A composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 199 to nucleotide 1155;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 304 to nucleotide 1155;
- (d) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone H963_20 deposited under accession number ATCC 98145;
- (e) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone H963_20 deposited under accession number ATCC 98145;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone H963_20 deposited under accession number ATCC 98145;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone H963_20 deposited under accession number ATCC 98145;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:28;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and
- (l) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(i).

35. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:28;
- (b) the amino acid sequence of SEQ ID NO:28 from amino acid 19 to amino acid 84;
- (c) fragments of the amino acid sequence of SEQ ID NO:28; and
- (d) the amino acid sequence encoded by the cDNA insert of clone H963_20 deposited under accession number ATCC 98145;

the protein being substantially free from other mammalian proteins.

36. The gene corresponding to the cDNA sequence of SEQ ID NO:27.